

ABSTRACT OF THE DISCLOSURE

Method and system to predict and optimize probe-target hybridization are provided. The method may be implemented using six interactive, interrelated, software modules. Module 1 predicts the hybridization thermodynamics of a duplex given the two strands. Module 2 finds the best primer of a given length binding to a given target. Module 3 executes a primer walk to find alternative binding sites of a given primer on a given target. Module 5 is a combination of Modules 2 and 3. Module 6 finds the alternative binding sites of a given primer on a given target (Module 3) and calculates the concentration of target with primer bound at primary and alternative sites. Module 7 is a combination of Modules 2 and 5 and also calculates the various concentrations. The six modules can be operated either through an interactive user interface or using batch file submission as provided by Module 4. The program is suited to predict DNA/DNA, RNA/RNA, and RNA/DNA systems.